

SCORE Search Results Details for Application 098833 and Search Result us-09-883-343a-19.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:50:07 ; Search time 512 Seconds
(without alignments)
2745.692 Million cell updates/sec

Title: US-09-883-343A-19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	53.2	31.3	13377	7	US-10-221-714A-198	Sequence 198, App
6	52.4	30.8	16914	7	US-10-221-613-214	Sequence 214, App
7	50.6	29.8	10762	7	US-10-240-589C-131	Sequence 131, App
8	50.6	29.8	11691	6	US-10-311-455-2214	Sequence 2214, Ap
9	50.2	29.5	3673778	6	US-10-312-841-2	Sequence 2, Appli
c 10	50	29.4	385	7	US-10-424-599-86585	Sequence 86585, A
11	50	29.4	467	7	US-10-021-323-6541	Sequence 6541, Ap
c 12	49.6	29.2	531	7	US-10-021-323-6375	Sequence 6375, Ap
13	49.6	29.2	5867	7	US-10-433-793-181	Sequence 181, App
14	49.4	29.1	531	7	US-10-021-323-6375	Sequence 6375, Ap
15	49.4	29.1	3673778	6	US-10-312-841-1	Sequence 1, Appli
c 16	49	28.8	539	8	US-10-425-115-172904	Sequence 172904,
17	49	28.8	2354	8	US-10-602-494-100	Sequence 100, App
18	49	28.8	2354	8	US-10-602-494-242	Sequence 242, App
c 19	48.8	28.7	469	7	US-10-021-323-16830	Sequence 16830, A
20	48.8	28.7	194883	5	US-10-087-192-826	Sequence 826, App
21	48.6	28.6	359	3	US-09-814-353-17359	Sequence 17359, A
22	48.6	28.6	9106	6	US-10-240-452-70	Sequence 70, Appl
23	48.6	28.6	14006	6	US-10-311-455-1932	Sequence 1932, Ap
c 24	48.4	28.5	486	7	US-10-021-323-16008	Sequence 16008, A
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26	48.4	28.5	13814	6	US-10-311-455-1165	Sequence 1165, Ap
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31	47.8	28.1	6048	6	US-10-311-455-482	Sequence 482, App
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33	47.4	27.9	9204	6	US-10-311-455-1101	Sequence 1101, Ap
34	47.4	27.9	9204	7	US-10-221-613-153	Sequence 153, App
c 35	47.2	27.8	277	3	US-09-960-352-12673	Sequence 12673, A
36	47.2	27.8	539	3	US-09-814-353-17862	Sequence 17862, A
c 37	47	27.6	325	8	US-10-425-115-55801	Sequence 55801, A
38	47	27.6	587	8	US-10-425-115-91618	Sequence 91618, A
39	47	27.6	6823	6	US-10-311-455-1117	Sequence 1117, Ap
40	47	27.6	7113	6	US-10-311-455-778	Sequence 778, App
41	47	27.6	12592	7	US-10-221-613-57	Sequence 57, Appl
42	47	27.6	15373	6	US-10-311-455-439	Sequence 439, App
43	46.8	27.5	499	7	US-10-021-323-10189	Sequence 10189, A
44	46.8	27.5	549	7	US-10-021-323-7101	Sequence 7101, Ap
45	46.8	27.5	6029	7	US-10-240-589C-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-09-883-343A-19

; Sequence 19, Application US/09883343A

; Publication No. US20030039632A1

GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.

; APPLICANT: Vederas, John C.

; APPLICANT: van Belkum, Marius J.

; APPLICANT: Worobo, Randy W.

; APPLICANT: Worobo, Rodney J.

; APPLICANT: Greer, G. Gordon

; APPLICANT: McMullen, Lynn M.

; APPLICANT: Leisner, Jorgen J.

; APPLICANT: Poon, Alsion

; APPLICANT: Franz, Charles M.A.P.

; TITLE OF INVENTION: No. US20030039632A1elBacteriocins, Transport and Vector System and Metho

; FILE REFERENCE: 660.0005US

; CURRENT APPLICATION NUMBER: US/09/883,343A

; CURRENT FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US/08/924,629

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; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/026,257
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
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; TYPE: DNA
; ORGANISM: divergicin immunity gene;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(168)
; OTHER INFORMATION:
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US-09-883-343A-15

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; Sequence 15, Application US/09883343A
; Publication No. US20030039632A1
; GENERAL INFORMATION:
; APPLICANT: Stiles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
; APPLICANT: Worobo, Randy W.
; APPLICANT: Worobo, Rodney J.
; APPLICANT: Greer, G. Gordon
; APPLICANT: McMullen, Lynn M.
; APPLICANT: Leisner, Jorgen J.
; APPLICANT: Poon, Alston
; APPLICANT: Franz, Charles M.A.P.
; TITLE OF INVENTION: No. US20030039632A1elBacteriocins, Transport and Vector System and Metho
; FILE REFERENCE: 660.0005US
; CURRENT APPLICATION NUMBER: US/09/883,343A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/08/924,629
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/026,257
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3475
; TYPE: DNA
; ORGANISM: plasmid;
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Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a- 19.rnpbn.

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Perfect score: 170
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SUMMARIES

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c	7	44.4	26.1	615	7	US-09-925-065A-468837	Sequence 468837,
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	9	43.8	25.8	8252	17	US-11-011-332A-158	Sequence 158, App
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	17	43	25.3	3641	17	US-11-102-026A-181	Sequence 181, App
	18	43	25.3	5535	10	US-10-240-708-18	Sequence 18, Appl
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c	25	42.8	25.2	3328	7	US-09-925-065A-703954	Sequence 703954,
	26	42.6	25.1	11049	10	US-10-240-708-23	Sequence 23, Appl
	27	42.6	25.1	163317	17	US-11-117-187-212	Sequence 212, App
	28	42.4	24.9	1400	17	US-11-136-527-4311	Sequence 4311, Ap
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	35	42.2	24.8	19233	10	US-10-240-708-45	Sequence 45, Appl
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	41	42	24.7	601	7	US-09-925-065A-105820	Sequence 105820,
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US-10-932-182A-166169/c

; Sequence 166169, Application US/10932182A

; Publication No. US20060046253A1

GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rni.

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(without alignments)
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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	170	100.0	3475	3	US-08-924-629C-15	Sequence 15, Appl
3	48.8	28.7	178883	3	US-09-949-016-12733	Sequence 12733, A
4	48.8	28.7	178884	3	US-09-949-016-13039	Sequence 13039, A
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	9	43.6	25.6	63588	3	US-10-243-735-3	Sequence 3, Appli
	10	43.6	25.6	129658	3	US-09-949-016-17195	Sequence 17195, A
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	44	40.8	24.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
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ALIGNMENTS

RESULT 1

US-08-924-629C-19

; Sequence 19, Application US/08924629C

; Patent No. 6403082

; GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.

; APPLICANT: Vederas, John C.

; APPLICANT: van Belkum, Marius J.

; APPLICANT: Worobo, Randy W.

; APPLICANT: Worobo, Rodney J.

; APPLICANT: Greer, G. Gordon

; APPLICANT: McMullen, Lynn M.

; APPLICANT: Leisner, Jorgen J.

; APPLICANT: Poon, Alsion

; APPLICANT: Franz, Charles M.A.P.

; TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method of Use

; FILE REFERENCE: 660.0005US

; CURRENT APPLICATION NUMBER: US/08/924,629C

; CURRENT FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 60/026,257

; PRIOR FILING DATE: 1996-09-05

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 170
; TYPE: DNA
; ORGANISM: divergicin immunity gene;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(168)
; OTHER INFORMATION:
US-08-924-629C-19

Query Match 100.0%; Score 170; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-08-924-629C-15

; Sequence 15, Application US/08924629C
; Patent No. 6403082
; GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
; APPLICANT: Worobo, Randy W.
; APPLICANT: Worobo, Rodney J.
; APPLICANT: Greer, G. Gordon
; APPLICANT: McMullen, Lynn M.
; APPLICANT: Leisner, Jorgen J.
; APPLICANT: Poon, Alston
; APPLICANT: Franz, Charles M.A.P.
; TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method of Use
; FILE REFERENCE: 660.0005US
; CURRENT APPLICATION NUMBER: US/08/924,629C
; CURRENT FILING DATE: 1997-09-05
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; NUMBER OF SEQ ID NOS: 80
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; ORGANISM: plasmid;
US-08-924-629C-15

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Best Local Similarity 100.0%; Pred. No. 1.5e-24;
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SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rng.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:29:58 ; Search time 305 Seconds
(without alignments)
3714.747 Million cell updates/sec

Title: US-09-883-343A-19
Perfect score: 170
Sequence: 1 atgaaaataaaatggtactg.....tataaaaagataaacaata 170

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match Length DB ID Description

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	2	170	100.0	170	2	AAX17722	Aax17722 Divergici
	3	170	100.0	3475	2	AAV11696	Aav11696 Plasmid p
	4	170	100.0	3475	2	AAX17720	Aax17720 Food-grad
c	5	56.4	33.2	416	8	ABX39419	Abx39419 Bovine ES
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	8	52.4	30.8	16914	6	ABL70316	Abl70316 Chemicall
	9	52.4	30.8	16914	6	AAS61254	Aas61254 Human gen
	10	50.6	29.8	6118	6	ABN80110	Abn80110 Human che
	11	50.6	29.8	10762	6	ABL92322	Abl92322 Chemicall
	12	50.6	29.8	11691	6	ABL34241	Abl34241 Human imm
	13	50	29.4	467	13	ACN51760	Acn51760 Cotton an
c	14	49.6	29.2	531	13	ACN51594	Acn51594 Cotton an
	15	49.6	29.2	5867	6	ABQ67151	Abq67151 Human ang
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	21	48.6	28.6	359	5	ADL43469	Adl43469 Human ova
	22	48.6	28.6	9106	6	ABL54370	Abl54370 Chemicall
	23	48.6	28.6	14006	6	ABL33959	Abl33959 Human imm
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	25	48.4	28.5	13814	6	ABL33192	Abl33192 Human imm
c	26	48.4	28.5	335913	5	AAI61371	Aai61371 Soybean 2
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	28	47.8	28.1	608	5	ADL37588	Adl37588 Human ova
	29	47.8	28.1	608	5	ADI72448	Adi72448 Human ova
	30	47.8	28.1	6048	6	ABL32509	Abl32509 Human imm
	31	47.8	28.1	24939	6	ABL70570	Abl70570 Chemicall
	32	47.4	27.9	5464	6	AAS63342	Aas63342 Chemicall
	33	47.4	27.9	9204	6	ABL33128	Abl33128 Human imm
	34	47.4	27.9	9204	6	ABK31292	Abk31292 Signal tr
	35	47.4	27.9	9204	6	ABL70269	Abl70269 Chemicall
	36	47.4	27.9	9204	6	AAS61194	Aas61194 Human gen
c	37	47.2	27.8	277	8	ABX47508	Abx47508 Bovine ES
c	38	47.2	27.8	435	4	AAI82079	Aai82079 Human pol
	39	47.2	27.8	539	5	ADL43972	Adl43972 Human ova
	40	47	27.6	6823	6	ABL33144	Abl33144 Human imm
	41	47	27.6	7113	6	ABL32805	Abl32805 Human imm
	42	47	27.6	12592	6	AAS61101	Aas61101 Human gen
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	44	46.8	27.5	499	13	ACN55408	Acn55408 Cotton an
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ALIGNMENTS

RESULT 1

AAV11698

ID AAV11698 standard; DNA; 170 BP.

XX

AC AAV11698;

XX

DT 25-MAR-2003 (revised)

DT 14-SEP-1998 (first entry)

XX

DE Divergicin immunity gene.

XX

KW Divergicin; bacteriocin; signal peptide; protein secretion; preservative;

KW food spoilage; lactic acid bacterium; antibacterial; immunity gene; ss.

XX

OS Carnobacterium divergens.

XX

XX

PD 12-MAR-1998.

XX

PF 05-SEP-1997; 97WO-US015609.

XX

PR 05-SEP-1996; 96US-0026257P.

XX

PA (UYAL-) UNIV ALBERTA.

XX

PI Stiles ME, Vederas JC, Van Belkum MJ, Worobo RW, Worobo RJ;

PI McCormick JK, Greer GG, McMullen LM, Leisner JJ, Pkns J, Poon A;

PI Franz CM;

XX

DR WPI; 1998-193319/17.

DR P-PSDB; AAW59019.

XX

PT Bacterial growth inhibiting peptide(s) enterocin 900 or brochocin C -

PT used to inhibit growth of susceptible bacteria in e.g. foodstuff, living

PT animal, food preparation area or fermentation vessel.

XX

PS Disclosure; Page 130; 174pp; English.

XX

CC This DNA sequence comprises the divergicin immunity gene of the meat
CC lactic acid bacterium, *Carnobacterium divergens*. It codes for a 56-amino
CC acid protein (see AAW59019) that protects the host organism against
CC divergicin. The invention provides a secretion vector in which the
CC structural and immunity genes of other bacteriocins, such as
CC carnobacteriocin B2 (see AAW59029-31), colicin V, leucocin A and
CC brochocin-C (see AAW59021), are fused to the divergicin A signal peptide
CC (see AAW59010) gene sequence, allowing production and secretion of the
CC bacteriocin(s) by host and heterologous bacteria. Bacteriocin cassettes
CC encoding the divergicin signal peptide and two or more bacteriocins are
CC used to tailor the antibacterial spectrum of a producer strain to target
CC a range of spoilage or pathogenic bacteria, e.g. *Escherichia coli* and
CC *Salmonella*. Using the technology of multiple bacteriocin production and
CC delivery using lactic acid bacteria, a range of bacteriocins can be
CC produced in situ in human food, animal feed, the gastrointestinal tract
CC of humans and animals, and in the female genital tract. (Updated on 25-
CC MAR-2003 to correct PI field.)

XX

SQ Sequence 170 BP; 59 A; 12 C; 23 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 170; DB 2; Length 170;

Best Local Similarity 100.0%; Pred. No. 5.4e-21;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTTGTATTTTTTTATAGAAGTTCTGGTTTTCTTTAAAAAATTAGTTTTAGGAAGTTTA 120

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Db 61 CTTGTATTTTTTTATAGAAGTTCTGGTTTTCTTTAAAAAATTAGTTTTAGGAAGTTTA 120

Qy 121 TTTTATTTGATAGCAATTGGTCTTTTAAATTATAAAAAGATAAACAAATA 170

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Db 121 TTTTATTTGATAGCAATTGGTCTTTTAAATTATAAAAAGATAAACAAATA 170

RESULT 2

AAX17722

ID AAX17722 standard; DNA; 170 BP.

XX

AC AAX17722;

XX

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 7	54.4	32.0	90347	5	AL714030	AL714030 Zebrafish
c 8	54.4	32.0	99681	5	AL713850	AL713850 Zebrafish
c 9	54.4	32.0	160905	5	BX571969	BX571969 Zebrafish
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13	52.4	30.8	16914	6	AX251953	AX251953 Sequence
14	52.4	30.8	16914	6	AX348748	AX348748 Sequence
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c 16	52.2	30.7	252394	2	AE014833	AE014833 Plasmodiu
17	52	30.6	128352	15	AC144591	AC144591 Medicago
18	52	30.6	135950	14	CR848821	CR848821 Danio rer
19	51.8	30.5	4910	2	AF465313	AF465313 Dictyoste
20	51.8	30.5	39984	2	AC114258	AC114258 Dictyoste
c 21	51.8	30.5	257109	2	AC116963	AC116963 Dictyoste
c 22	51.6	30.4	251551	2	AE014844	AE014844 Plasmodiu
c 23	51.2	30.1	242710	14	AC138733	AC138733 Pongo pyg
24	51.2	30.1	331039	2	AC116979	AC116979 Dictyoste
25	51	30.0	154071	2	AC115598	AC115598 Dictyoste
26	51	30.0	165892	5	AL929516	AL929516 Zebrafish
c 27	51	30.0	170534	14	CR391918	CR391918 Danio rer
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c 43	49.6	29.2	215018	14	AC139113	AC139113 Pongo pyg
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ALIGNMENTS

RESULT 1

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LOCUS AR212585 170 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 19 from patent US 6403082.
 ACCESSION AR212585
 VERSION AR212585.1 GI:23309309
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 170)
 AUTHORS Stiles,M.E., Vederas,J.C., Van Belkum,M.J., Worobo,R.W.,
 Worobo,R.J., McCormick,J.K., Greer,G.G., McMullen,L.M.,
 Leisner,J.J., Poon,A. and Franz,C.M.A.P.
 TITLE Bacteriocins, transport and vector system and method of use thereof

JOURNAL Patent: US 6403082-A 19 11-JUN-2002;

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RESULT 2

BD006997

LOCUS BD006997 170 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel bacteriocins, transport and vector system and method of use thereof.

ACCESSION BD006997

VERSION BD006997.1 GI:18635368

KEYWORDS JP 2001503970-A/5.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 170)

AUTHORS Stiles,M.E., Vederasu,J.C., Berukumu,M.J.V., Worobo,R.W.,
Worobo,R.J., McCormick,J.K., Gordon,G.G., McMallen,L.M.,
Reizuneru,J.J., Poone,A. and Frantz,C.M.A.P.

TITLE Novel bacteriocins, transport and vector system and method of use

JOURNAL Patent: JP 2001503970-A 5 27-MAR-2001;
GOVERNORS OF THE UNIVERSITY OF ALBERTA

COMMENT OS Unidentified

PN JP 2001503970-A/5

PD 27-MAR-2001

PF 05-SEP-1997 JP 1998512914

PR 05-SEP-1996 US 60/026257

PI MICHAEL E STILES,JOHN C VEDERASU,MARIUS J VAN BERUKUMU, PI

RODNEY W WOROBO,

PI RODNEY J WOROBO,JOHN K MCCORMICK,GRIER G GORDON, PI LYNN M
MCMALLEN,

PI JORGEN J REIZUNERU,ALISON POONE,CHARLES M A P FRANTZ PC

C12N15/09,A01K37/18,A23L1/30,A23L1/305,A61K38/00,A61P31/00, PC

A61P31/04,

PC C07K14/335,C07K16/12,C12N1/1/21,C12P21/02,C12P21/08,C12N15/00,

PC A61K37/02

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CC Topology: Linear;

FH Key Location/Qualifiers

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ORIGIN

SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rst.

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Maximum Match 100%
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

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SUMMARIES

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c 3	55.2	32.5	168	1	AU074456	AU074456 AU074456	

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c	7	53	31.2	240	1	AU071622	AU071622 AU071622
	8	53	31.2	1201	10	CNS0167M	AL106396 Drosophil
c	9	52.6	30.9	805	11	CNS06V7I	AL416788 T7 end of
c	10	52.4	30.8	929	9	CC391046	CC391046 PUHHD32TB
	11	52.4	30.8	978	8	DN563011	DN563011 87653490
	12	52.2	30.7	927	9	AZ046250	AZ046250 nbab0091D
	13	51.6	30.4	530	5	BX566754	BX566754 BX566754
c	14	51.6	30.4	600	8	DN351463	DN351463 LIB3579-0
	15	51.4	30.2	1200	10	CNS0162Z	AL106229 Drosophil
c	16	51.2	30.1	187	1	AU071758	AU071758 AU071758
	17	51.2	30.1	926	3	BM394635	BM394635 50072-2-5
	18	51.2	30.1	970	10	CNS0182E	AL108800 Drosophil
	19	51.2	30.1	1023	8	DN568261	DN568261 90172339
	20	51	30.0	240	1	AU072475	AU072475 AU072475
c	21	51	30.0	540	7	CO885816	CO885816 BovGen_14
	22	51	30.0	947	10	CZ524990	CZ524990 GMW2-62N1
c	23	51	30.0	986	8	DN575739	DN575739 90182439
c	24	50.6	29.8	340	8	DN863041	DN863041 nab40d08.
c	25	50.6	29.8	1044	10	CNS005D6	AL058139 Drosophil
c	26	50.6	29.8	1101	10	CNS003DX	AL064587 Drosophil
c	27	50.4	29.6	767	10	CNS00AQX	AL055924 Drosophil
	28	50.4	29.6	999	10	CW942426	CW942426 TcB23.4_G
c	29	50.4	29.6	1092	10	CNS020K7	AL175696 Tetraodon
c	30	50.4	29.6	1101	10	CNS00Z2U	AL097152 Drosophil
c	31	50.2	29.5	858	5	BU935417	BU935417 AGENCOURT
	32	50.2	29.5	1100	9	BZ696700	BZ696700 SP_Ba008
c	33	50.2	29.5	1383	10	CL510075	CL510075 SAIL_823_
c	34	50	29.4	313	5	BQ391420	BQ391420 NISC_mq18
c	35	49.8	29.3	506	8	DN353227	DN353227 LIB3580-0
	36	49.8	29.3	644	7	CV226785	CV226785 WS0165.B2
	37	49.8	29.3	1008	8	DN563433	DN563433 92240038
c	38	49.8	29.3	1101	10	CNS00ZBM	AL097468 Drosophil
	39	49.8	29.3	1160	8	DR732342	DR732342 FGAS07826
	40	49.6	29.2	709	8	DN137796	DN137796 ACAE-aaa0
	41	49.6	29.2	761	8	CX585478	CX585478 TTE000268
c	42	49.6	29.2	905	10	CNS00KHX	AL077798 Drosophil
c	43	49.4	29.1	162	2	BI268723	BI268723 NF023E03G
	44	49.4	29.1	230	5	BX473837	BX473837 DKFZp686H
	45	49.4	29.1	230	8	DN892016	DN892016 naol7g08.

ALIGNMENTS

RESULT 1

DN572350/c

LOCUS DN572350 1004 bp mRNA linear EST 14-MAR-2005

DEFINITION 92239480 Sea Urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PMCSRP2-166A11 3', mRNA
sequence.

ACCESSION DN572350

VERSION DN572350.1 GI:61131389

KEYWORDS EST.

SOURCE Strongylocentrotus purpuratus

ORGANISM Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 1004)

AUTHORS Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
Ettensohn,C.A.

TITLE A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo

JOURNAL Development 128 (13), 2615-2627 (2001)
 PUBMED 11493577
 COMMENT Contact: Erica Sodergren
 Human Genome Sequencing Center
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713-798-7676
 Fax: 713-798-6977
 Email: ericas@bcm.tmc.edu
 NCBI Trace Archive: 486722151
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FEATURES
 source Location/Qualifiers
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 /organism="Strongylocentrotus purpuratus"
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 /db_xref="taxon:7668"
 /clone="PMCSPR2-166A11"
 /tissue_type="embryo"
 /cell_type="primary mesenchyme cells"
 /lab_host="E.coli"
 /clone_lib="Sea Urchin primary mesenchyme cell cDNA library"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: MluI; oligo
 dt priming from poly A+ RNA, directionally cloned"

ORIGIN

Query Match 34.9%; Score 59.4; DB 8; Length 1004;
 Best Local Similarity 60.0%; Pred. No. 0.65;
 Matches 99; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 5 AAATAAAATGGTACTGGAATCTCTGATTGAAACCTTAATATTTATAATTGTTCTTCTTG 64
 || ||||| || | | | | | | | | | | | | | | | |
 Db 521 AATTAAGGGAATTTTAATTTTAAATTTACAAAATTAATTAATTTTATTTTATTTT 462
 Qy 65 TATTTTTTTATAGAAGTCTGGTTTTCTTTAAAAATTTAGTTTATAGGAAGTTTATTTT 124
 | ||||| | | | | | | | | | | | | | | | | |
 Db 461 TTTTTTTTAAAAAAATTTTATTTTTTTTTTAAACCCTTTTTTTTTTAAAAATTTT 402
 Qy 125 ATTTGATAGCAATTGGTCTTTTTTAATTATAAAAAGATAAACAAAT 169
 | | | | | | | | | | | | | | | | | | | |
 Db 401 AAAAAAATTATCTTTTTTTTACACTAAATTAAAAAAT 357

RESULT 2

CNS00AIS/c
 LOCUS CNS00AIS 783 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR21G10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL055833
 VERSION AL055833.1 GI:4936400
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 783)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).